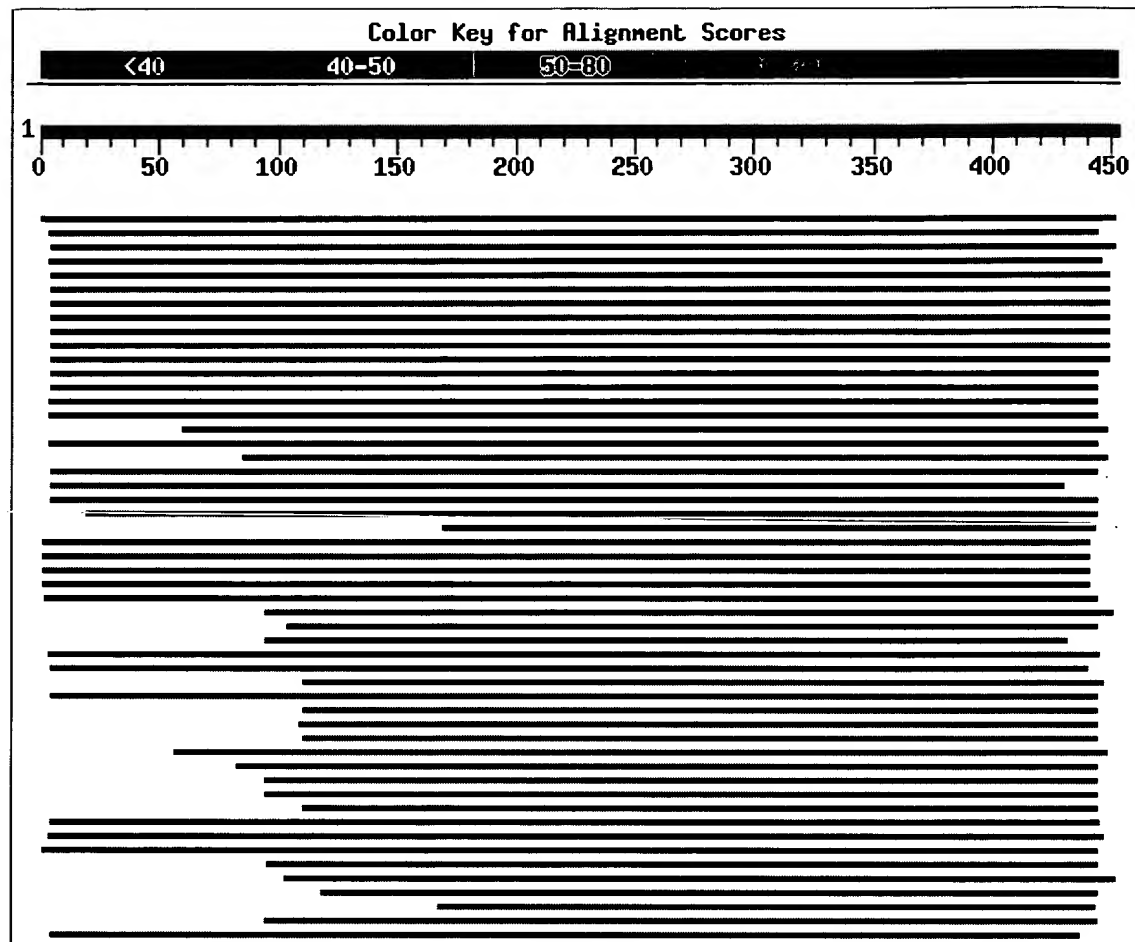


$$\begin{matrix} 1 & 6 & 2 & 2 \\ & 2 & & \end{matrix}$$



Sequences producing significant alignments:

Score E
(bits) Value

gi	2501490	sp	Q96493	UFOG GENTR	FLAVONOL 3-O-GLUCOSYLTRANSF...	844	0.0
gi	4455123	gb	AAD21086.1		(AF127218) flavonoid 3-O-glucosyl...	433	e-120
gi	1944201	dbj	BAA19659.1		(AB002818) flavonoid 3-O-glucosy...	417	e-115
gi	15237899	ref	NP 197207.1		UDP glucose:flavonoid 3-o-gluc...	413	e-114
gi	13620861	dbj	BAB41020.1		(AB047093) UDP-glucose:flavonoi...	402	e-111
gi	13620869	dbj	BAB41024.1		(AB047097) UDP-glucose:flavonoi...	402	e-111
gi	13620855	dbj	BAB41017.1		(AB047090) UDP-glucose:flavonoi...	400	e-110
gi	13620859	dbj	BAB41019.1		(AB047092) UDP-glucose:flavonoi...	400	e-110
gi	2564112	gb	AAB81682.1		(AF000371) UDP glucose:flavonoid ...	395	e-109
gi	2564114	gb	AAB81683.1		(AF000372) UDP glucose:flavonoid ...	394	e-109
gi	13620857	dbj	BAB41018.1		(AB047091) UDP-glucose:flavonoi...	393	e-108
gi	6683050	dbj	BAA89008.1		(AB027454) anthocyanidin 3-O-glu...	392	e-108
gi	5917676	gb	AAD55985.1	AF165148.1	(AF165148) UDP-galactos...	372	e-102
gi	15237895	ref	NP 197205.1		UDP glucose:flavonoid 3-o-gluc...	366	e-100
gi	6634776	gb	AAF19756.1	AC009917.15	(AC009917) Contains si...	344	1e-93
gi	7489292	pir	T08005		flavonol 3-O-glucosyltransferase (EC...	343	1e-93
gi	15221434	ref	NP 174341.1		UDP glucose:flavonoid 3-o-gluc...	341	9e-93
gi	6983839	dbj	BAA90787.1		(AB038248) UDP glucose: flavonoi...	339	3e-92
gi	4588779	gb	AAD26203.1	AF117267.1	(AF117267) UDP glucose:...	338	7e-92
gi	2501498	sp	Q43641	UFOG SOLME	FLAVONOL 3-O-GLUCOSYLTRANSF...	338	8e-92
gi	4140026	dbj	BAA36972.1		(AB009370) flavonoid 3-O-galacto...	312	4e-84
gi	15237897	ref	NP 197206.1		UDP glucose:flavonoid 3-o-gluc...	309	4e-83
gi	2501496	sp	Q40289	UFO7 MANES	FLAVONOL 3-O-GLUCOSYLTRANSF...	279	5e-74
gi	136743	sp	P16166	UFO1 MAIZE	FLAVONOL 3-O-GLUCOSYLTRANSFE...	226	3e-58
gi	13241668	gb	AAK16410.1	AF320086.2	(AF320086) UDPG-flavon...	226	3e-58

gi	136744	sp	P16165	UFO2 MAIZE	FLAVONOL 3-O-GLUCOSYLTRANSFE...	220	2e-56
gi	136745	sp	P16167	UFO3 MAIZE	FLAVONOL 3-O-GLUCOSYLTRANSFE...	219	6e-56
gi	136746	sp	P14726	UFOG HORVU	FLAVONOL 3-O-GLUCOSYLTRANSFE...	207	2e-52
gi	8885562	dbj	BAA97492.1	(AB025604)	glucuronosyl transfer...	180	2e-44
gi	15238467	ref	NP 200767.1		glucuronosyl transferase - lik...	175	9e-43
gi	15238465	ref	NP 200766.1		glucuronosyl transferase - lik...	174	1e-42
gi	7385017	gb	AAF61647.1	AF190634 1	(AF190634) UDP-glucose:...	173	4e-42
gi	15228063	ref	NP 181234.1		putative glucosyltransferase [...	170	3e-41
gi	15219876	ref	NP 173656.1		UDP-glucose glucosyltransferas...	167	2e-40
gi	6683052	dbj	BAA89009.1	(AB027455)	anthocyanin 5-O-gluco...	165	1e-39
gi	15219870	ref	NP 173653.1		UDP-glucose glucosyltransferas...	164	1e-39
gi	15624034	dbj	BAB68088.1	(AP003560)	putative flavonol gl...	162	8e-39
gi	15218268	ref	NP 177950.1		UDP-glucose glucosyltransferas...	161	1e-38
gi	15232620	ref	NP 190253.1		glucuronosyl transferase-like ...	160	2e-38
gi	15081809	gb	AAK82559.1	(AY048297)	AT3g46660/F12A12_180 ...	158	1e-37
gi	15232619	ref	NP 190252.1		glucosyltransferase-like prote...	158	1e-37
gi	15232600	ref	NP 190250.1		glucosyltransferase-like prote...	158	1e-37
gi	15219867	ref	NP 173652.1		UDP-glucose glucosyltransferas...	157	2e-37
gi	15225138	ref	NP 180738.1		putative glucosyltransferase [...	155	8e-37
gi	15221233	ref	NP 172059.1		putative indole-3-acetate beta...	154	1e-36
gi	15234619	ref	NP 193285.1		indole-3-acetate beta-glucosyl...	153	4e-36
gi	15220950	ref	NP 173655.1		UDP-glucose glucosyltransferas...	152	4e-36
gi	629669	pir	S39507	glucuronosyl transferase homolog, rip...	152	5e-36	
gi	4115559	dbj	BAA36421.1	(AB013596)	UDP-glucose:anthocysn...	152	8e-36
gi	7488834	pir	T06371	probable UDP-glucuronosyltransferase...	152	9e-36	
gi	15232618	ref	NP 190251.1		glucosyltransferase-like prote...	150	2e-35
gi	15229731	ref	NP 187742.1		glucosyl transferase, putative...	150	2e-35
gi	15240825	ref	NP 198620.1		glucosyltransferase-like prote...	150	2e-35
gi	15219871	ref	NP 173654.1		UDP-glucose glucosyltransferas...	149	4e-35
gi	15226332	ref	NP 180375.1		putative glucosyltransferase [...	149	5e-35
gi	4115563	dbj	BAA36423.1	(AB013598)	UDP-glucose:anthocyan...	149	7e-35
gi	15225134	ref	NP 180734.1		putative glucosyltransferase [...	149	8e-35
gi	15221232	ref	NP 172058.1		putative indole-3-acetate beta...	148	8e-35
gi	15228174	ref	NP 191129.1		glucuronosyl transferase - lik...	147	2e-34
gi	14192682	gb	AAK54465.1	(AY033489)	cold-induced glucosyl...	147	2e-34
gi	15624036	dbj	BAB68090.1	(AP003560)	putative flavonol gl...	146	3e-34
gi	15234616	ref	NP 193284.1		indole-3-acetate beta-glucosyl...	146	4e-34
gi	15227610	ref	NP 180534.1		putative flavonol 3-O-glucosyl...	146	4e-34
gi	15239288	ref	NP 196209.1		glucuronosyl transferase-like ...	146	5e-34
gi	15239259	ref	NP 196207.1		glucuronosyl transferase-like ...	145	9e-34
gi	15233091	ref	NP 188793.1		UDP-glucose:indole-3-acetate b...	144	2e-33
gi	5763524	dbj	BAA83484.1	(AB031274)	UDP-glucose: flavonoi...	144	2e-33
gi	15228031	ref	NP 181213.1		putative glucosyl transferase ...	143	4e-33
gi	15240822	ref	NP 198617.1		glucosyltransferase-like prote...	142	6e-33
gi	9794913	gb	AAF98390.1	AF287143 1	(AF287143) UDP-glucose:...	141	1e-32
gi	15232623	ref	NP 190256.1		glucuronosyl transferase-like ...	141	2e-32
gi	2501495	sp	Q40288	UFO6 MANES	FLAVONOL 3-O-GLUCOSYLTRANSF...	140	2e-32
gi	15232598	ref	NP 190249.1		glucosyltransferase-like prote...	140	2e-32
gi	15228033	ref	NP 181215.1		putative glucosyl transferase ...	140	2e-32
gi	15220559	ref	NP 172047.1		UDP-glucose:indole-3-acetate b...	140	3e-32
gi	15228037	ref	NP 181218.1		putative glucosyl transferase ...	140	4e-32
gi	8778722	gb	AAF79730.1	AC005106 11	(AC005106) T25N20.21 [...	139	5e-32
gi	7433911	pir	T07404	probable glucosyltransferase twil (E...	139	5e-32	
gi	15224368	ref	NP 181910.1		putative glucosyltransferase [...	139	6e-32
gi	15227717	ref	NP 180576.1		putative glucosyltransferase [...	137	1e-31
gi	15232621	ref	NP 190254.1		glucuronosyl transferase-like ...	137	2e-31
gi	15228034	ref	NP 181216.1		putative glucosyl transferase ...	137	2e-31
gi	12322891	gb	AAG51429.1	AC008153 2	(AC008153) putative UD...	137	2e-31
gi	2149127	gb	AAB58497.1	(U81293)	UDP-glucose:indole-3-ace...	137	2e-31
gi	11994646	dbj	BAB02841.1	(AB025634)	UTP-glucose glucosyl...	137	3e-31
gi	15233157	ref	NP 188816.1		putative UDP-glucose glucosylt...	136	5e-31
gi	13431605	sp	Q9MB73	LGT CITUN	LIMONOID UDP-GLUCOSYLTRANSF...	136	5e-31
gi	1717967	sp	P51094	UFOG VITVI	FLAVONOL 3-O-GLUCOSYLTRANSF...	135	5e-31
gi	7433906	pir	T03747	glucosyltransferase IS5a (EC 2.4.1.-...	135	5e-31	
gi	13492674	gb	AAK28303.1	AF346431 1	(AF346431) phenylpropa...	135	5e-31

gi	15227796	ref	NP_179907.1	putative glucosyltransferase [...	135	9e-31
gi	15240305	ref	NP_198003.1	UTP-glucose glucosyltransferas...	135	1e-30
gi	4115561	dbj	BAA36422.1	(AB013597) UDP-glucose:anthocyan...	134	1e-30
gi	7433904	pir	T02238	glucosyl transferase, jasmonate-indu...	134	1e-30
gi	15234630	ref	NP_193290.1	glucosyltransferase like prote...	134	2e-30
gi	15235245	ref	NP_195139.1	glucosyltransferase -like prot...	134	3e-30
gi	15228032	ref	NP_181214.1	putative glucosyl transferase ...	133	4e-30
gi	7433905	pir	T03745	glucosyltransferase IS10a (EC 2.4.1....	132	4e-30
gi	13492676	gb	AAK28304.1	AF346432.1 (AF346432) phenylpropa...	132	5e-30
gi	2501494	sp	Q40287	UFO5 MANES FLAVONOL 3-O-GLUCOSYLTRANSF...	132	6e-30

Alignments

>gi|2501490|sp|Q96493|UFOG GENTR FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVO
3-O-GLUCOSYLTRANSFERASE)

gi|1620013|dbj|BAA12737.1| (D85186) UDP-glucose:flavonoid-3-glucosyltransferase [Ge
triflora]

Length = 453

Score = 844 bits (2180), Expect = 0.0

Identities = 424/453 (93%), Positives = 424/453 (93%)

Query: 1 MSPVSHVAVLAFPGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXXPTNLISIGS 60
MSPVSHVAVLAFPGTHAAPLLTLVNRLAASAPD PTNLISIGS

Sbjct: 1 MSPVSHVAVLAFPGTHAAPLLTLVNRLAASAPDIIFSFFSTSSSITTIFSPTNLISIGS 60

Query: 61 NIKPYAVWDGSPGEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFL 120
NIKPYAVWDGSPGEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFL

Sbjct: 61 NIKPYAVWDGSPGEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFL 120

Query: 121 WFAADFSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEFDIAEKAECTIDFIPGLSAI 180
WFAADFSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEFDIAEKAECTIDFIPGLSAI

Sbjct: 121 WFAADFSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEFDIAEKAECTIDFIPGLSAI 180

Query: 181 SFSDLPEELIMEDSQSIFALT LHNMG LKLHKATAVAVNSFEEIDPIITNHLRSTNQLNIL 240
SFSDLPEELIMEDSQSIFALT LHNMG LKLHKATAVAVNSFEEIDPIITNHLRSTNQLNIL

Sbjct: 181 SFSDLPEELIMEDSQSIFALT LHNMG LKLHKATAVAVNSFEEIDPIITNHLRSTNQLNIL 240

Query: 241 NIGPLQTLSSSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIP 300
NIGPLQTLSSSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIP

Sbjct: 241 NIGPLQTLSSSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIP 300

Query: 301 FLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFC 360
FLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFC

Sbjct: 301 FLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFC 360

Query: 361 RVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNV 420
RVPVIGRPFFGDQKVNARMVED FTEDETTRVLELVLFSDKGKEMRQNV

Sbjct: 361 RVPVIGRPFFGDQKVNARMVEDVWKIGVGKGGVFTEDETTRVLELVLFSDKGKEMRQNV 420

Query: 421 GRLKEKAKDAVKANGSSTRNFESLLAAFNLDS 453
GRLKEKAKDAVKANGSSTRNFESLLAAFNLDS

Sbjct: 421 GRLKEKAKDAVKANGSSTRNFESLLAAFNLDS 453

>gi|4455123|gb|AAD21086.1| (AF127218) flavonoid 3-O-glucosyltransferase [Forsythia x
intermedia]

Length = 454

Score = 433 bits (1113), Expect = e-120

Identities = 228/444 (51%), Positives = 297/444 (66%), Gaps = 6/444 (1%)

Query: 5 SHVAVLAFPGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXXPTNLISIGSNIKP 64
SH+ VLAFFPGTHAAPLLTLV RL + NIK

Sbjct: 5 SHIGVLAFFPGTHAAPLLTLVRRRLVLDSSSQGITFSFFNTAKSNCAIFSG--QEFDNIKA 62

Query: 65 YAVWDGSPGEGFVFSG-NPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWFA 123
 Y VWDG+ EG F+G N E ++ FL A P NF+K MK+A G+ ISCLL+DAFLWF
 Sbjct: 63 YDWDGTGHEGEAFTGSNILEAMQLFLAATPGNFKEKVMKEAEVKNMGKISCLLSDAFLWFT 122

Query: 124 ADFSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEFDIAEKAECTIDFIPGLSAISFS 183
 D +E+ G+PW+ WTAASCSL H+YTD+I S A+ EKT+ F+PG++++ FS
 Sbjct: 123 CDLAEERGIPWVSFWTAASCSLSAHMYTDQIWSLMRSTGTAKTEEKTLSFVPGMTSVRFS 182

Query: 184 DLPEELIMEDSQSIFALT LHNMG LKLHKATAVAVNSFEEIDPIITNHLRSTNQLNLNIG 243
 DLPEE++ ++ +S L ++ M KL K+TA+ VNSFEEIDP+ITN L+S Q N LNIG
 Sbjct: 183 DLPEEILSDNLESPLTLMIYKMQKLSKSTAIVVNSFEEIDPVITNDLKSFKQ-NFLNIG 241

Query: 244 PLQTLSSSIPPEDN--ECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIPF 301
 P S ++ D+ ECL WL+ Q+ +SV+Y+SFGTVI P P EMA LA LE+ + PF
 Sbjct: 242 PSILSSPTLSNGDSGQECLLWLEKQRHASVIYISFGTVITPQPREMAGLAEALLETGEFPF 301

Query: 302 LWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCR 361
 LWSLRD A K LP+ F+DRTS FG IVSWAPQL VLENP++G F+THCGWNS LESI
 Sbjct: 302 LWSLRDNAMKLLPDGFLDRTSKFGMIVSWAPQLKVLENPSVGAFITHCGWNSTLESISFG 361

Query: 362 VPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNVG 421
 VP+I RPPFGDQ +N++MVED FT++ T L V+ ++ GK +R+N+
 Sbjct: 362 VPMICRPFFGDQNLNSKMVEDVWKIGVRLEGGVFTKNGTIEALHSVMLNETGKAIRENIN 421

Query: 422 RLKEKAKDAVKANGSSSTRNFESLL 445
 +LK KA++AVK +G+ST+NF +LL
 Sbjct: 422 KLKRKAQNAVKFDGTSTKNFRALL 445

>gi|1944201|dbj|BAA19659.1| (AB002818) flavonoid 3-O-glucosyltransferase [Perilla fr
 Length = 447

Score = 417 bits (1071), Expect = e-115

Identities = 220/451 (48%), Positives = 290/451 (63%), Gaps = 13/451 (2%)

Query: 6 HVAVLAFPPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIKPY 65
 H+ VLAFFPFGTHA PLL LV RLAAS+P NI+ +
 Sbjct: 6 HIGVLAFPPFGTHAPLLALVRRRLAASSPGTFLSFLNSAESNAALFNERTY----DNIRAF 61

Query: 66 AVWDGSPGEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWFAAD 125
 VWDG+PEG +F+G E + FL A+P NFDK +++A TG+ I CL+TDAFLWFA D
 Sbjct: 62 DVWDGTPEGRIFTGTHFEAVGLFLKASPGNFDKVIEEAEPKTGLKICCLITDAFLWFACD 121

Query: 126 FSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEFDIAEKAECTIDFIPGLSAISFSDL 185
 ++K G+PW+P WTAASCSL H+YTD+I E+ + FIPGL + +DL
 Sbjct: 122 MAQKRGLPWVPFWTAASCSLSSHLTYTDQIVKAG-----TANQEQLNSFIPGLEMATLTDL 176

Query: 186 PEELIMEDSQSIFALT LHNMG LKLHKATAVAVNSFEEIDPIITNHLRSTNQLNLNIGP- 244
 P E+ +++S S A+T++ M KL K+TAV +NSFEEIDPIIT+ L++ + N LN+GP
 Sbjct: 177 PPEVFLDNPSPLAITINKMVEKLPKSTAVVLSNFEEIDPIITDDLKTKFK-NFLNVGPS 235

Query: 245 -LQTLSSSIPPEDNECLKWLQTQKE-SSVVYLSFGTVINPPPNEMAALASTLESRKIPFL 302
 L + + P ++ CL WL Q SVVY+SFGTVI PP NE+AALA LE + PFL
 Sbjct: 236 ILASPPQATPDDETGCLSWLADQTSKSVVYISFGTVITPPENELAAALADALEICRFPFL 295

Query: 303 WSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRV 362
 WSL+D A K LP+ F+DRT FGKIV+WAPQ VL + +GVFVTHCGWNS LESI V
 Sbjct: 296 WSLKDYAVKSLPDGFLDRTKGFGKIVAWAPQQQVLAHRNVGVFVTHCGWNSILESISCV 355

Query: 363 PVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNVGR 422
 P+I RPPFGDQK+N+RMV+D FT++E L+ ++ ++ G ++R+NV
 Sbjct: 356 PLICRPFFGDQKLNSRMVQDSWKIGVRVEGGVFTKNEAVESLKKLMATEAGMKIRENVSL 415

Query: 423 LKEKAKDAVKANGSSSTRNFESLLAFAFNKLD 453
 L+EKA AVK GSS++NF+ LL +S
 Sbjct: 416 LREKATAAVKPEGSSSQNFKKLEIIGAAS 446

>gi|15237899|ref|NP_197207.1| UDP glucose:flavonoid 3-o-glucosyltransferase -like pr
 [Arabidopsis thaliana]
 gi|11358643|pir|T51560 probable flavonol 3-O-glucosyltransferase (EC 2.4.1.91) F2K
 [similarity] - Arabidopsis thaliana
 gi|9755706|emb|CAC01718.1| (AL391141) UDP glucose:flavonoid 3-o-glucosyltransferase
 protein [Arabidopsis thaliana]
 Length = 460

Score = 413 bits (1062), Expect = e-114

Identities = 209/446 (46%), Positives = 283/446 (62%), Gaps = 4/446 (0%)

Query: 5 SHVAVLAFPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIKP 64
 SHVAVLAFPFGTHAAPLLT+ RLA+++P + +NI+
 Sbjct: 11 SHVAVLAFPFGTHAAPLLTVTRRLASASPSTVFSFFNTAQSNSSLFSSGDEADRPANIRV 70

Query: 65 YAVWDGSPEGFVFSGNPREDIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWFAA 124
 Y + DG PEG+VFSG P+E IE FL AAP+NF + + KA + G + CL+TDAF WFAA
 Sbjct: 71 YDIADGVPEGYVFSGRPQEAIELFLQAAPENFRREIAKAETEVGTEVKCLMTDAFFWFAA 130

Query: 125 DFSEKIGVPWIPVWTAASCSLCHVYTDEIRSRFAEFDIAEKAECTIDFIPGLSAISFSD 184
 D + +I WI WTA + SL H+YTD IR ++ E+ E+TI I G+ I D
 Sbjct: 131 DMATEINASWIAFWTAGANSLSAHLYTDLIRETIGVKEVGERMEETIGVISGMEKIRVKD 190

Query: 185 LPEELIMEDSQSIFALT LHNMG LKLHKATAVAVNSFEEIDPIITNHLRSTNQLNINIGP 244
 PE ++ + S+F+ LH MGL L +ATAV +NSFE++DP +TN+LRS + LNIGP
 Sbjct: 191 TPEGVVFGNLDSVFSKMLHQMGLALPRATAVFINSFEDLPTLTNNLRSRFK-RYLNIGP 249

Query: 245 LQTLSSSIP---PEDNECLKWLQTKESSVVYLSFGTVINPPPNEMAALASTLESRKIPF 301
 L LSS++ + + CL W++ + SV Y+SFGTV+ PPP E+AA+A LES K+PF
 Sbjct: 250 LGLSSTLQQLVQDPHGCLAWMEKRSSGSVAYISFGTVMTPPPGELAAIAEGLESSKVPF 309

Query: 302 LWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCR 361
 +WSL++++ LP+ F+DRT G +V WAPQ+ +L++ A GV FVTHCGWNS LES+
 Sbjct: 310 VWSLKEKSLVQLPKGFLDRTREQGIVVPWAPQVELLKHEATGVFVTHCGWNSVLESVSGG 369

Query: 362 VPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLFSDKKGEMRQNVG 421
 VP+I RPPFFGDQ++N R VE FT+D + L+ VL D GK+M+ N
 Sbjct: 370 VPMICRPFFGDQRLNGRAVEVVWEIGMTIINGVFTKDGFEKCLDKVLVQDDGKKMKCNK 429

Query: 422 RLKEKAKDAVKANGSSSTRNFESLLAA 447
 +LKE A +AV + G S+ NF LL A
 Sbjct: 430 KLKELAYEAVSSKGRSSENFRGLLDA 455

>gi|13620861|dbj|BAB41020.1| (AB047093) UDP-glucose:flavonoid 3-O-glucosyltransferas
 vinifera]
 gi|13620865|dbj|BAB41022.1| (AB047095) UDP-glucose:flavonoid 3-O-glucosyltransferas
 vinifera]
 Length = 456

Score = 402 bits (1034), Expect = e-111

Identities = 212/446 (47%), Positives = 289/446 (64%), Gaps = 3/446 (0%)

Query: 6 HVAVLAFPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIKP 65
 HVAVLAFPF THAAPLL +V RLAA+AP + + ++ NIK Y
 Sbjct: 9 HVAVLAFPFSTHAAPLLAVVRRRLAAAAPHAVFSFFSTSQSNASIFHDS-MHTMQCNIKSY 67

Query: 66 AVWDGSPEGFVFSGNPREDIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWFAAD 125
 V DG PEG+VF+G P+E IE F+ AAP++F + M AV +TG +SCL+ DAF+WFAAD
 Sbjct: 68 DVSDGVPEGYVFAGRPQEDIELFMRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAD 127

Query: 126 FSEKIGVPWIPVWTAASCSLCHVYTDEIRSRFAEFDIAEKAECTIDFIPGLSAISFSDL 185
 + ++GV W+P WTA SL HVYTDEIR + I + ++ ++FIPG+S + F DL
 Sbjct: 128 MAAEMGVAWLPFWTAGPNSLSTHVYTDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDL 187

Query: 186 PEELIMEDSQSIFALTLHNMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILNIGPL 245
 E ++ + S+F+ LH MG L KATAV +NSFEE+D +TN L+S + LNIGP
 Sbjct: 188 QEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLKSCLK-TYLNIGPF 246

Query: 246 QTLS-SSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWS 304
 ++ + P CL+WL+ +K +SVVY+SFGTV PPP E+ ALA LE+ ++PF+WS
 Sbjct: 247 NLITPPPVIPNTTGCLQWLKERKPTSVVYISFGTVTPPPAELVALAEAEASRVPFWS 306

Query: 305 LRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRVPV 364
 LRD+AR HLPE F+++T +G +V WAPQ VL + A+G FVTHCGWNS ES+ VP+
 Sbjct: 307 LRDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPL 366

Query: 365 IGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDTTRVLELVLFSDKGKEMRQNVGRLK 424
 I RPPFFGDQ++N RMVED FTE+ +L +KGK++R+N+ L+
 Sbjct: 367 ICRPFFGDQRLNGRMVEDALEIGVRIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALR 426

Query: 425 EKAKDAVKANGSSTRNFESLLAAFNK 450
 E A AV GSST NF++L+ +K
 Sbjct: 427 ETADRAVGPKGSSTENFKTLVDLVSK 452

>gi|13620869|dbj|BAB41024.1| (AB047097) UDP-glucose:flavonoid 3-O-glucosyltransferas
 vinifera]
 gi|13620873|dbj|BAB41026.1| (AB047099) UDP-glucose:flavonoid 3-O-glucosyltransferas
 vinifera]
 Length = 456

Score = 402 bits (1032), Expect = e-111

Identities = 211/446 (47%), Positives = 289/446 (64%), Gaps = 3/446 (0%)

Query: 6 HVAVLAFPFPGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIKPY 65
 HVAVLAFPF THAAPLL +V RLAA+AP + + ++ NIK Y
 Sbjct: 9 HVAVLAFPFSTHAAPLLAVVRRLLAAAAPHAVFSFFSTSQSNASIFHDS-MHTMQCNIKSY 67

Query: 66 AVWDGSPGEGFVFGSGNPREDIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWFAAD 125
 + DG PEG+VF+G P+E IE F+ AAP++F + M AV +TG +SCL+ DAF+WFAAD
 Sbjct: 68 DISDGVPEGYVFAGRPQEDIELFMRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAD 127

Query: 126 FSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEFDIAEKAETIDFIPGLSAISFSDL 185
 + ++GV W+P WTA SL HVYTDEIR + I + ++ ++FIPG+S + F DL
 Sbjct: 128 MAAEMGVAVLFPFWTAGPNSLSTHVYTDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDL 187

Query: 186 PEELIMEDSQSIFALTLHNMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILNIGPL 245
 E ++ + S+F+ LH MG L KATAV +NSFEE+D +TN L+S + LNIGP
 Sbjct: 188 QEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLKSCLK-TYLNIGPF 246

Query: 246 QTLS-SSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWS 304
 ++ + P CL+WL+ +K +SVVY+SFGTV PPP E+ ALA LE+ ++PF+WS
 Sbjct: 247 NLITPPPVIPNTTGCLQWLKERKPTSVVYISFGTVTPPPAELVALAEAEASRVPFWS 306

Query: 305 LRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRVPV 364
 LRD+A HLPE F+++T +G +V WAPQ VL + A+G FVTHCGWNS ES+ VP+
 Sbjct: 307 LRDKASVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPL 366

Query: 365 IGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDTTRVLELVLFSDKGKEMRQNVGRLK 424
 I RPPFFGDQ++N RMVED FTE+ +L +KGK++R+N+ L+
 Sbjct: 367 ICRPFFGDQRLNGRMVEDALEIGVRIEGGVFTENGLMSCFDQILSQEKGKKLRENLRALR 426

Query: 425 EKAKDAVKANGSSTRNFESLLAAFNK 450
 E A AV GSST NF++L+ +K
 Sbjct: 427 ETADRAVGPKGSSTENFKTLVDLVSK 452

>gi|13620855|dbj|BAB41017.1| (AB047090) UDP-glucose:flavonoid 3-O-glucosyltransferas
 labrusca x Vitis vinifera]
 Length = 456

Score = 400 bits (1028), Expect = e-110
 Identities = 211/446 (47%), Positives = 288/446 (64%), Gaps = 3/446 (0%)

Query: 6 HVAVLAFPPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIKP 65
 HVAVLAFPF THAAPLL +V RLAA+AP + + ++ NIK Y
 Sbjct: 9 HVAVLAFPFSTHAAPLLAVVRLAAAAPHAVFSFFSTSESNASISHDS-MHTMQCNIKSY 67

Query: 66 AVWDGSPEGFVFSGNPREDIEYFLNAAPDNFDKAMKKAEDTGVNISCLLTDAFLWFAAD 125
 V DG PEG+VF+G P+E IE F+ AAP++F + M AV +TG +SCL+ DAF+WFAAD
 Sbjct: 68 DVSDGVPEGYVFAGRPQEDIELFMRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAD 127

Query: 126 FSEKIGVPWIPVWTAASCSLCLHVTDEIRSRFAEFDIAEKAECTIDFIPGLSAISFSDL 185
 + ++GV W+P WTA SL HVTDEIR + I + ++ ++FIPG+ + F DL
 Sbjct: 128 MAAEMGVAWLPFWTAGPNSLSTHVTDEIREKIGVSGIQGREDELLNFIPGMYEVRFRDL 187

Query: 186 PEELIMEDSQSIFALT LHNMG LKHKATAVAVNSFEEIDPIITNHLRSTNQLNINIGPL 245
 E ++ + S+F+ LH MG L KATAV +NSFEE+D +TN L+S + LNIGP
 Sbjct: 188 QEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLKSCLK-TYLNIGPF 246

Query: 246 QTLS-SSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWS 304
 ++ + P CL+WL+ +K +SVVY+SFGTV PPP E+ ALA LE+ ++PF+WS
 Sbjct: 247 NLITPPPVVPPNTTGCLQWLKERKPTSVVYISFGTVTPPPAELVALAEAEASRVPFWS 306

Query: 305 LRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSLTLESIFCRVPV 364
 LRD+AR HLPE F+++T +G +V WAPQ VL + A+G FVTHCGWNS ES+ VP+
 Sbjct: 307 LRDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPL 366

Query: 365 IGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDTTRVLELVLFSDKGKEMRQNVGRK 424
 I RPPFFGDQ++N RMVED FT+ +L +KGK++R+N+ L+
 Sbjct: 367 ICRPFFGDQRLNGRMVEDVLEIGVRIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALR 426

Query: 425 EKAKDAVKANGSSSTRNFESLLAAFNK 450
 E A AV GSST NF++L+ +K
 Sbjct: 427 ETADRAVGPKGSSTENFKTLVDLVSK 452

>gi|13620859|dbj|BAB41019.1| (AB047092) UDP-glucose:flavonoid 3-O-glucosyltransferase
 vinifera]
 gi|13620863|dbj|BAB41021.1| (AB047094) UDP-glucose:flavonoid 3-O-glucosyltransferase
 vinifera]
 gi|13620867|dbj|BAB41023.1| (AB047096) UDP-glucose:flavonoid 3-O-glucosyltransferase
 vinifera]
 gi|13620871|dbj|BAB41025.1| (AB047098) UDP-glucose:flavonoid 3-O-glucosyltransferase
 vinifera]
 Length = 456

Score = 400 bits (1028), Expect = e-110
 Identities = 211/446 (47%), Positives = 287/446 (64%), Gaps = 3/446 (0%)

Query: 6 HVAVLAFPPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIKP 65
 HVAVLAFPF THAAPLL +V RLAA+AP + + ++ NIK Y
 Sbjct: 9 HVAVLAFPFSTHAAPLLAVVRLAAAAPHAVFSFFSTSESNASISHDS-MHTMQCNIKSY 67

Query: 66 AVWDGSPEGFVFSGNPREDIEYFLNAAPDNFDKAMKKAEDTGVNISCLLTDAFLWFAAD 125
 + DG PEG+VF+G P+E IE F AAP++F + M AV +TG +SCL+ DAF+WFAAD
 Sbjct: 68 DISDGVPEGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAD 127

Query: 126 FSEKIGVPWIPVWTAASCSLCLHVTDEIRSRFAEFDIAEKAECTIDFIPGLSAISFSDL 185
 + ++GV W+P WTA SL HVY DEIR + I + ++ ++FIPG+S + F DL
 Sbjct: 128 MAAEMGVAWLPFWTAGPNSLSTHVTDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDL 187

Query: 186 PEELIMEDSQSIFALT LHNMG LKHKATAVAVNSFEEIDPIITNHLRSTNQLNINIGPL 245
 E ++ + S+F+ LH MG L KATAV +NSFEE+D +TN L+S + LNIGP
 Sbjct: 188 QEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLKSCLK-TYLNIGPF 246

Query: 246 QTLS-SSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWS 304


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      ++   + P   CL+WL+ +K +SVVY+SFGTV PPP E+ ALA LE+ ++PF+WS
Sbjct: 247 NLITPPPVVPNTTGCQLWLKERKPTSVVYISFGTVTTPPPAELVALAEALEASRVPFIFS 306

Query: 305 LRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRVPV 364
      LRD+AR HLPE F+++T +G +V WAPQ VL + A+G FVTHCGWNS ES+ VP+
Sbjct: 307 LRDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPL 366

Query: 365 IGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDTTRVLELVLFSDKGKEMRQNVGRLK 424
      I RPFFGDQ++N RMVED FTE + +L +KGK++R+N+ L+
Sbjct: 367 ICRPFFGDQRLNGRMVEDALEIGVRIEGGVFTESGLMSCFDQILSQEKGKKLRENLRALR 426

Query: 425 EKAKDAVKANGSSTRNFESLLAAFNK 450
      E A AV GSST NF++L+ +K
Sbjct: 427 ETADRAVGPKGSSTENFKTLVDLVSK 452

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>gi|2564112|gb|AAB81682.1| (AF000371) UDP glucose:flavonoid 3-o-glucosyltransferase
 vinifera]
 Length = 452

Score = 395 bits (1016), Expect = e-109

Identities = 209/446 (46%), Positives = 286/446 (63%), Gaps = 3/446 (0%)

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Query: 6   HVAVLAFPPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIKPY 65
      HVAVLAFPF THAAPLL +V RLAA+AP + + ++ NIK Y
Sbjct: 5   HVAVLAFPFSTHAAPLLAVVRRLLAAAAPHAVFSFFSTSQSNASIFHDS-MHTMQCNIKSY 63

Query: 66  AVWDGSPGEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWFAAD 125
      + DG PEG+VF+G P+E IE F AAP++F + M AV +TG +SCL+ DAF+WFAAD
Sbjct: 64  DISDGVPEGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAAD 123

Query: 126 FSEKIGVPWIPVWTAASCSLCHVYTDEIRSRFAEFDIAEKAECTIDFIPGLSAISFSDL 185
      + ++GV W+P WTA SL HVY DEIR + I + ++ ++FIPG+S + F DL
Sbjct: 124 MAAEMGVAWLPPFWTAGPNSLSSTHVYIDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDL 183

Query: 186 PEELIMEDSQSIFALT LHNMGKLKHKATAVAVNSFEEIDPIITNHLRSTNQLNINIGPL 245
      E ++ + S+F+ LH MG L KATAV +NSFEE+D +TN L+S + LNIGP
Sbjct: 184 QEGIVFGNLSLSFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLKSCLK-TYLNIGPF 242

Query: 246 QTLS-SSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWS 304
      ++   + P   CL+WL+ +K +SVVY+SFGTV PPP E+ AL+ LE+ ++PF+WS
Sbjct: 243 NLITPPPVVPNTTGCQLWLKERKPTSVVYISFGTVTTPPPAEVVALSEALEASRVPFIFS 302

Query: 305 LRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRVPV 364
      LRD+AR HLPE F+++T +G +V WAPQ VL + A+G FVTHCGWNS ES+ VP+
Sbjct: 303 LRDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPL 362

Query: 365 IGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDTTRVLELVLFSDKGKEMRQNVGRLK 424
      I RPFFGDQ++N RMVED FT+ + +L +KGK++R+N+ L+
Sbjct: 363 ICRPFFGDQRLNGRMVEDVLEIGVRIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALR 422

Query: 425 EKAKDAVKANGSSTRNFESLLAAFNK 450
      E A AV GSST NF +L+ +K
Sbjct: 423 ETADRAVGPKGSSTENFITLVDLVSK 448

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>gi|2564114|gb|AAB81683.1| (AF000372) UDP glucose:flavonoid 3-o-glucosyltransferase
 vinifera]
 Length = 456

Score = 394 bits (1013), Expect = e-109

Identities = 208/446 (46%), Positives = 286/446 (63%), Gaps = 3/446 (0%)

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Query: 6   HVAVLAFPPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIKPY 65
      HVAVLAFPF THAAPLL +V RLAA+AP + + ++ NIK Y
Sbjct: 9   HVAVLAFPFSTHAAPLLAVVRRLLAAAAPHAVFSFFSTSQSNASIFHDS-MHTMQCNIKSY 67

```

Query: 66 AVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAIVEDTGVNISCLLTDAFLWFAAD 125
+ DG PEG+VF+G P+E IE F AAP++F + M AV +TG +SCL+ DAF+WFAAD
Sbjct: 68 DISDGVPEGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAAD 127

Query: 126 FSEKIGVPWIPVWTAASCSLCHLVYTDEIRSRFAEFDIAEKAECTIDFIPGLSAISFSDL 185
+ ++G+ W+P WTA SL HVY DEIR + I + ++ ++FIPG+S + F DL
Sbjct: 128 MAAEMGLAWLPFWTAGPNSLSHVYIDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDL 187

Query: 186 PEELIMEDSQSIFALTTLHNMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILNIGPL 245
E ++ + S+F+ LH MG L KATAV +NSFEE+D +TN L+S + LNIGP
Sbjct: 188 QEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELEDDSLTNDLKSCLK-TYLNIGPF 246

Query: 246 QTLS-SSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWS 304
++ + P CL+WL+ +K +SVVY+SFGTV PPP E+ AL+ LE+ ++PF+WS
Sbjct: 247 NLITPPPVPNTTGCCLQWLKERKPTSVVYISFGTVITPPPAEVVALSEALEASRVPFWS 306

Query: 305 LRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRVPV 364
LRD+AR HLPE F+++T +G +V WAPQ VL + A+G FVTHCGWNS ES+ VP+
Sbjct: 307 LRDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPL 366

Query: 365 IGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNVGRLLK 424
I RPPFFGDQ++N RMVED FT+ + +L +KGK++R+N+ L+
Sbjct: 367 ICRPFFGDQRLNGRMVEDVLEIGVRIEGGVFTKSGLMSCFDQILSQEKGGKLRNLRLR 426

Query: 425 EKAKDAVKANGSSTRNFESLLAAFNK 450
E A AV GSST NF +L+ +K
Sbjct: 427 ETADRAVGPKGSSTENFITLVDLVSK 452

>gi|13620857|dbj|BAB41018.1| (AB047091) UDP-glucose:flavonoid 3-O-glucosyltransferase
labrusca x Vitis vinifera]
Length = 456

Score = 393 bits (1010), Expect = e-108

Identities = 209/446 (46%), Positives = 285/446 (63%), Gaps = 3/446 (0%)

Query: 6 HVAVLAFPPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIKP 65
HVAVLAFPPF THAAPLL +V RLAA+AP + + ++ NIK Y
Sbjct: 9 HVAVLAFPPFSTHAAPLLAVVRRLLAAAAPHAVFSFFSTSQSNASIFHDS-MHTMQCNISY 67

Query: 66 AVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAIVEDTGVNISCLLTDAFLWFAAD 125
V DG PEG+VF+G P+E IE F+ AAP++F + M AV +TG +SCL+ DAF+WFAAD
Sbjct: 68 DVSDGVPEGYVFAGRPQEDIELFMRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAAD 127

Query: 126 FSEKIGVPWIPVWTAASCSLCHLVYTDEIRSRFAEFDIAEKAECTIDFIPGLSAISFSDL 185
+ ++GV W+P WTA SL HVY DEIR + I + ++ ++FIPG+S + F DL
Sbjct: 128 MAAEMGVAWLPFWTAGPNSLSHVYIDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDL 187

Query: 186 PEELIMEDSQSIFALTTLHNMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILNIGPL 245
E ++ + S+F+ H MG L KATAV +NSFEE+D +TN L+S + LNIGP
Sbjct: 188 QEGIVFGNLNSLFSRMPHRMGQVLPKATAVFINSFEELEDDSLTNDLKSCLK-TYLNIGPF 246

Query: 246 QTLS-SSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWS 304
++ + P CL+WL+ +K +SVVY+SFGTV PPP E+ ALA LE+ ++PF+WS
Sbjct: 247 NLITPPPVPNTTGCCLQWLKERKPTSVVYISFGTVITPPPAEVVALAEALEASRVPFWS 306

Query: 305 LRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRVPV 364
LRD+AR HLPE F+++T G +V WAPQ VL + A+G FVTHCGWNS ES+ VP+
Sbjct: 307 LRDKARVHLPEGFLEKTRGHGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPL 366

Query: 365 IGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNVGRLLK 424
I RPPFFGDQ++N RMVED FT+ + +L +KGK++R+N+ L+
Sbjct: 367 ICRPFFGDQRLNGRMVEDVLEIGVRIEGGVFTKSGLMSCFDQILSQEKGGKLRNLRLR 426

Query: 425 EKAKDAVKANGSSTRNFESLLAAFNK 450
E A A GSST NF++L+ +K

Sbjct: 427 ETADRAAGPKGSSTENFKTLVDFVSK 452

>gi|6683050|dbj|BAA89008.1| (AB027454) anthocyanidin 3-O-glucosyltransferase [Petunia hybrida]
Length = 448

Score = 392 bits (1006), Expect = e-108
Identities = 220/453 (48%), Positives = 284/453 (62%), Gaps = 33/453 (7%)

Query: 6 HVAVLAFPPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGS---NI 62
H+A+LAFPPG+HAAPLLTLV +L+ P T++ S GS NI
Sbjct: 7 HIALLAFFPGSHAAPLLTLVQKLSFPLSDTIFSFFNTSQSN-----TSIFSEGSKPDNI 61

Query: 63 KPYAVWDGSPGFGVFSGNPR---EPIEYFLNAAPDNFDKAMKKAIVEDTGVNISCLLTDAF 119
K Y VWDG E +GN E I+ F+ A P NF+K MK+A E+TGV SC+ +DAF
Sbjct: 62 KVINVDGVTET---NGNKPVGLEAIKLFIQATPTNFEKVMKEAEEETGVKFSCIFSDAF 118

Query: 120 LWFAADFSEKIGVPWIPVWTAASCSLCLHVTDEIRSRFAEFDIAEKAECTIDFIPGLSA 179
LWF+ +EKI VPWI WTAAS SL +H+YTD IRS ++T IPG S+
Sbjct: 119 LWFSYKLAEKINVPWIAFWTAASGSLSVHLYTDFIRSN-----DETSLNIPGFSS 168

Query: 180 -ISFSDLPEELIMEDSQSIFALTLHNMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLN 238
+ SD+P E++ E+ L+NM L LHKA AV +NSFEE+DP I L+ Q
Sbjct: 169 TLKISDMPPEVMAENLDLPMPSMLYNMALNLHKA AAVVLNSFEELDPTINKDLKVKLQ-K 227

Query: 239 ILNIGPLQTLSSSIPP-----EDNECLKWLQTQKESSVVYLSFGTVINPPPNEAALAS 292
+LNIGPL L + P ++ C+ WL+ QKE SVVYLSFGTV PPNE+ A+A
Sbjct: 228 VLNIGPL-VLQPTSPKKVLDACDERGCIWLEKQKESSVVYLSFGTVTTLPNEIVAVAE 286

Query: 293 TLESRKIPFLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWN 352
LE++K PF+WSL+D K+LP F++RT FGKIVSWAPQL +L + A+GVFVTHCGWN
Sbjct: 287 ALEAKKFPFIWSLKDNIGIKNLPTGFLERTGQFGKIVSWAPQLEILNHSAGVVFVTHCGWN 346

Query: 353 STLESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDTTRVLELVLFSDK 412
S LE I C VP+I RPFFGDQK+N+RMVE FT+ T L+ +K
Sbjct: 347 SILEGISCGVPMICRPFFGDQKLN SRMVESVWQIGLQIEGGSFTKIGTISALDTFFSEEK 406

Query: 413 GKEMRQNVGRLKEKAKDAVKANGSSTRNFESLL 445
GK +R+NV LKE+A +AVK +GSS++NF+ L+
Sbjct: 407 GKVLRNVKGLKERALEAVKPDGSSSKNFKDLV 439

>gi|5917676|gb|AAD55985.1|AF165148.1 (AF165148) UDP-galactose:flavonol 3-O-galactosyltransferase [Petunia x hybrida]
Length = 451

Score = 372 bits (956), Expect = e-102
Identities = 200/447 (44%), Positives = 268/447 (59%), Gaps = 14/447 (3%)

Query: 6 HVAVLAFPPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIKP 65
HVAVLAFPP THA LL LV RLA + P+ + +NIKP+
Sbjct: 5 HVAVLAFPPFATHAGLLLGLVQRLANALPNVTFTFFNTSKSNSSLFTTPH----DNNIKPF 60

Query: 66 AVWDGSPGFGVF-SGNPREPIEYFLNAAPDNFDKAMKKAIVEDTGVNISCLLTDAFLWFAA 124
+ DG PEG+V G I F +A +N AM AVE++G I+C++ DAF+WF+
Sbjct: 61 NISDGVPEGYVVGKGGIEALIGLFFKSAKENIQNAMA AVEESGKKITCVMADAFMWFSG 120

Query: 125 DFSEKIGVPWIPVWTAASCSLCLHVTDEIRSRFAEFDIAEKAECTIDFIPGLSAISFSD 184
+ +E++ V WIP+WTA+ SL +HVYTD IR IA + ++ + FIPG + +
Sbjct: 121 EIAEELSVGWIPLWTSAGSLSVHVTDLIRENVEAQGIAGREDEILTFIPGFAELRLGS 180

Query: 185 LPEELIMEDSQSIFALTLHNMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILNIGP 244
LP ++ D +S F++ LH MG + KATA+ VNSFEE+DP I L+S N LN+GP
Sbjct: 181 LPSGVVSGDLESPPFSVMLHMGKTIGKATALPVNSFEELDPPIVEDLKS KFN-NFLNVGP 239

Query: 245 LQTLSSSIPPEDN-----ECLKWLQTQKESSVVYLSFGTVINPPPNEAALASTLESRKI 299

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      ++ PP N      C+ WL Q+ SV Y+ FGTV PPPNE+ A+A LE K
Sbjct: 240 FNL--TTPPPSANITDEYGCIAWLKQEPGVSAYIGFGTVATPPPNELKAMAEALEESKT 297

Query: 300 PFLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIF 359
      PFLWSL+D + PE F++RTS +GKIVSWAPQ+ VL + ++GVF+ HCGWNS LESI
Sbjct: 298 PFLWSLKDLFKSFFPEGFLERTSEYGKIVSWAPQVQVLSHGSGVGFVHCGWNSVLESIA 357

Query: 360 CRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLFSDK-GKEMRQ 418
      VPVI RPPFGD ++NA MVE FT+D T L+LVL DK E++Q
Sbjct: 358 AGVPVICRPFFGDHQLNAWMVEKVKIGVKIEGGVFTKDGTMALDLVLSKDKRNTTELKQ 417

Query: 419 NVGRLKEKAKDAVKANGSSTRNFESLL 445
      +G KE A +AV +GSS NF+ L+
Sbjct: 418 QIGMYKELALNAVGPSGSSAENFKKL 444

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>gi|15237895|ref|NP_197205.1| UDP glucose:flavonoid 3-o-glucosyltransferase -like pr
      [Arabidopsis thaliana]
gi|11358641|pir|T51558 probable flavonol 3-O-glucosyltransferase (EC 2.4.1.91) F2K
      [similarity] - Arabidopsis thaliana
gi|9755704|emb|CAC01716.1| (AL391141) UDP glucose:flavonoid 3-o-glucosyltransferase
      protein [Arabidopsis thaliana]
      Length = 459

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Score = 366 bits (939), Expect = e-100

Identities = 198/449 (44%), Positives = 270/449 (60%), Gaps = 15/449 (3%)

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Query: 5 SHVAVLAFPPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLIS--IGSNI 62
      SHVAVL FPFGTHAAPLL + RLA +AP ++L+S I +NI
Sbjct: 11 SHVAVLVFPFGTHAAPLLAVTCRLATAAPSTVFSFFSTARSN-----SSLLSSDIPTNI 64

Query: 63 KPYAVWDGSPGEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWF 122
      + + V DG PEGFV +GNP+ +E FL AAP+ F + +K A + G C+LTDAFLW
Sbjct: 65 RVHNVDDGVPEGFVLTGNPQHAVELFLEAAPEIFRREIKAAETEVRKFKCILTDAFLWL 124

Query: 123 AADF-SEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEFDIAEKAETIDFIPGLSAIS 181
      AA+ + ++ W+ + + SL H+YTD IR ++ E+ E+TI FI G+ I
Sbjct: 125 AAETAAEMKASWVAYYGGGATSLTAHLYTDAIRENVGVKEVGERMEETIGFISGMEKIR 184

Query: 182 FSDLPEELIMEDSQSIFALTTLHNMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILN 241
      D E ++ + S+F+ TLH MGL L +ATAV +NSFEE+DP TN RS + LN
Sbjct: 185 VKDTQEGVVFGNLDSVFSKTLHQMLALPRATAVFINSFEELDPTFTNDFRSEFK-RYLN 243

Query: 242 IGPLQTLS-----SSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLES 296
      IGPL LS S++ + + CL W++ + +SV Y++FG V PPP E+ A+A LES
Sbjct: 244 IGPLALLSSPSQTSTLVHDPHGCLAWIEKRSTASVAYIAFGRVATPPPVELVAIAQGLES 303

Query: 297 RKIPFLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLE 356
      K+PF+WSL++ HLPE F+DRT G +V WAPQ+ +L + A+GVFV+H GWNS LE
Sbjct: 304 SKVPFVWSLQEMKMTLHPEGFLDRTREQGMVVPWAPQVELLNHEAMGVFVSHGGWNSVLE 363

Query: 357 SIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEM 416
      S+ VP+I RP FGD +NAR VE FT+D L+ VL D GK+M
Sbjct: 364 SVSAGVPMICRPIFGDHAINARSVEAVWEIGVTISSGVFTKDGFEESLDRVLVQDDGKKM 423

Query: 417 RQNVGRLKEKAKDAVKANGSSTRNFESLL 445
      + N +L+E A++AV GSS NF LL
Sbjct: 424 KVNAKKLEELAQAESTKGSSSFENFGGLL 452

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>gi|6634776|gb|AAF19756.1|AC009917_15 (AC009917) Contains similarity to gb|AF000372
      3-o-glucosyltransferase from Vitis vinifera, and is a
      member of the UDP-gulcoronosyl and UDP-glucosyl
      transferase family PF|00201. ESTs gb|AA586155,
      gb|T45239 come from this gene. [Ar>
gi|13430496|gb|AAK25870.1|AF360160_1 (AF360160) putative UDP-gulcoronosyl and UDP-g
      family protein [Arabidopsis thaliana]

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gi|15810547|gb|AAL07161.1| (AY056312) putative UDP-gulcoronosyl and UDP-glucosyl tr
family protein [Arabidopsis thaliana]
Length = 453

Score = 344 bits (882), Expect = 1e-93
Identities = 187/445 (42%), Positives = 258/445 (57%), Gaps = 12/445 (2%)

Query: 5 SHVAVLA-FPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIK 63
SHVAVLA FP G HA PLL + RLAA++P + NIK
Sbjct: 11 SHVAVLAFFPVGAGHAGPLLA VTRRLAAASPSTIFSFFNTARSNASLFSSDH----PENIK 66

Query: 64 PYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWFA 123
+ V DG PEG + GNP E +E FL AAP F + A + G ++C+LTDAF WFA
Sbjct: 67 VHDVSDGVPEGTML-GNPLEMVLFLEAAPRIFRSEIAAAEIEVGKKVTCMLTDAFFWFA 125

Query: 124 ADFSEKIGVPWIPVWTAASCSLCLHVTDEIRSRFAEFDIAEKAECTIDFIPGLSAISFS 183
AD + ++ W+ W + SLC H+YTD IR D++ E+T+ FIPG+
Sbjct: 126 ADIAAELNATWVAFWAGGANS LCAHLYTDLIRETIGLKDVS--MEETLGFIPGMENYRVK 183

Query: 184 DLPEELIMEDSQSIFALT LHNMG LK LHKATAVAVNSFEEIDPIITNHLRSTNQLNILNIG 243
D+PEE++ ED S+F L+ M L L +A+AV ++SFEE++P + +LRS + LNI
Sbjct: 184 DIPEEVFEDLDSVFPKALYQMSLALPRASAVFISSFEELEPTLNYNLRSKLK-RFLNIA 242

Query: 244 PLQTLSSSIPPEDNE---CLKWLQTQKESSVYLSFGTVINPPPNEMAALASTLESRKIP 300
PL LSS+ E + C W+ + +SV Y+SFGTV+ PPP E+ A+A LES K+P
Sbjct: 243 PLTLLSSTSEKEMRDPHGCFAWMGKRSAA SVAYISFGTVMEPPPEELVAIAQGLESSKVP 302

Query: 301 FLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFC 360
F+WSL+++ HLP+ F+DRT G +V WAPQ+ +L++ A+GV VTHCGWNS LES+
Sbjct: 303 FVWSLKEKNMVHLPKGFLDRTREQGIVVPWAPQVELLKHEAMGVNVTHCGWNSVLESVSA 362

Query: 361 RVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNV 420
VP+IGRP D ++N R VE FT++ + L V D GK M+ N
Sbjct: 363 GVPMIGRPILADNRLNGRAVEVWVKGVMMDNGVFTKEGFEKCLNDVFVHDDGKTMKANA 422

Query: 421 GRLKEKAKDAVKANGSSSTRNFESLL 445
+LKEK ++ GSS NF+ LL
Sbjct: 423 KKLKEKLQEDFSMKGSSLENFKILL 447

>gi|7489292|pir|T08005 flavonol 3-O-glucosyltransferase (EC 2.4.1.91) - common
morning-glory (fragment)
gi|2599054|gb|AAB86473.1| (AF028237) UDP glucose: flavonoid 3-O-glucosyltransferase
purpurea]
Length = 420

Score = 343 bits (881), Expect = 1e-93
Identities = 177/400 (44%), Positives = 253/400 (63%), Gaps = 17/400 (4%)

Query: 61 NIKPYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFL 120
N+K Y VWDG+ G + E F+ A P N+ KA+ +A +TG C LTDAFL
Sbjct: 24 NVKAYDVWDGTVAGEALVTH-----EEFIMAMPGNVYKAI AEAEAEETGTFKGCFLTDAFL 78

Query: 121 WFAADF-SEKIGVPWIPVWTAASCSLCLHVTDEIRSRFAEFDIAEK--AEKTIDFIPGL 177
WF D +E+ GVPWI +WTA +CS+ H+YTD +RS A E+ + IPG+
Sbjct: 79 WFGGDLAAERGGVPWIALWTAGACISAHLYTDFVRS LAAATPTGNGNVLEQKLKVIPGM 138

Query: 178 SAISFSDLPEELIMEDSQSIFALT LHNMG LK LHKATAVAVNSFEEIDPIITNHLRSTNQL 237
S IS ++P E++ +D Q F ++NM LKL A AV +NSF+ ++P +T+ +RS Q
Sbjct: 139 SEISIGEMPGEILAKDLQEPFPGMIYNMALKLPGANAVVINSFQNL EPTVTDDIRSKLQ- 197

Query: 238 NILNIGPL----QTLSSSIPP--EDNECLKWLQTQKESS--VVYLSFGTVINPPPNEMAA 289
+ NIGP+ ++ PP +D+ C+ W+ + +S VYLSFG+ + PPP+E+ A
Sbjct: 198 KVFNIGPMILRQAAAATPKPPISDDHNCIPWVDSLPPASPPAVYLSFGSGLTPPPDEIVA 257

Query: 290 LASTLESRKIPFLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHC 349

LA LE+++ PFLWSL+ KHLPE F++RT FGKIV WAPQ+ VL +P +G FVTHC
 Sbjct: 258 LAEAELEAKRAPFLWSLKPHGVKHLPEGFLERTKEFGKIVPWAPQVQVLSHPGVGAFVTHC 317

Query: 350 GWNSTLESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLF 409
 GWNSTLE+I V +I RPF+GDQ++N+R VE FT+DET + + +VL

Sbjct: 318 GWNSTLEAISFGVCLICRPFYGDQQINSRFVESVWEIGVKVEGGKFTKDETLKAINVVLD 377

Query: 410 SDKGKEMRQNVGRLKEKAKDAVKANGSSTRNFESLLA AFN 449
 SD+GK +++NV +LK +A +AVK +GSST+ F+ L+ N

Sbjct: 378 SDRGKLLKENVVKLKGEAMEAVKPHGSSTKEFQELVHLLN 417

>gi|15221434|ref|NP_174341.1| UDP glucose:flavonoid 3-o-glucosyltransferase, putativ
 [Arabidopsis thaliana]
 Length = 450

Score = 341 bits (874), Expect = 9e-93
 Identities = 187/445 (42%), Positives = 256/445 (57%), Gaps = 15/445 (3%)

Query: 5 SHVAVLA-FPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIK 63
 SHVAVLA FP G HA PLL + RLAA++P + NIK

Sbjct: 11 SHVAVLAFFPVGAGHAGPLLAVTRRLAAASPSTIFSFFNTARSNASLFSSDH----PENIK 66

Query: 64 PYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWFA 123
 + V DG PEG + GNP E +E FL AAP F + A + G ++C+LTDAF WFA

Sbjct: 67 VHDVSDGVPEGTML-GNPLEMVELFLEAAPRIFRSEIAAAEIEVGKKVTCMLTDAFFWFA 125

Query: 124 ADFSEKIGVPWIPVWTAASCSLCLHVTDEIRSRFAEFDIAEKAETIDFIPGLSAISFS 183
 AD + ++ W+ W + SLC H+YTD IR I E+T+ FIPG+

Sbjct: 126 ADIAAELNATWVAFWAGGANSLSLAHYTDLIRE-----TIDVSMEETLGFIPGMENYRVK 180

Query: 184 DLPEELIMEDSQSIFALTTLHNMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILNIG 243
 D+PEE++ ED S+F L+ M L L +A+AV ++SFEE++P + +LRS + LNI

Sbjct: 181 DIPEEVVFEDLDSVFPKALYQMSLALPRASAVFISSFEELEPTLNYNLRSLK-LRFLNIA 239

Query: 244 PLQTLSSSIPPEDNE---CLKWLQTQKESSVYLSFGTVINPPPNEAALASTLESRKIP 300
 PL LSS+ E + C W+ + +SV Y+SFGTV+ PPP E+ A+A LES K+P

Sbjct: 240 PLTLLSSTSEKEMRDPHGCFAWMGKRSAAASVAYISFGTVMEPPPEELVAIAQGLESSKVP 299

Query: 301 FLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFC 360
 F+WSL+++ HLP+ F+DRT G +V WAPQ+ +L++ A+GV VTHCGWNS LES+

Sbjct: 300 FVWSLKEKNMVHLPKGFLDRTREQGIVVPWAPQVELLKHEAMGVNVTHCGWNSVLESVSA 359

Query: 361 RVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNV 420
 VP+IGRP D ++N R VE FT++ + L V D GK M+ N

Sbjct: 360 GVPMIGRPILADNRLNGRAVEVVWKVGVMMDNGVFTKEGFEKCLNDVFVHDDGKTMKANA 419

Query: 421 GRLKEKAKDAVKANGSSTRNFESLL 445
 +LKEK ++ GSS NF+ LL

Sbjct: 420 KKLKEKLQEDFSMKGSSLENFKILL 444

>gi|6983839|dbj|BAA90787.1| (AB038248) UDP glucose: flavonoid 3-O-glucosyltransferas
 batatas]
 Length = 383

Score = 339 bits (870), Expect = 3e-92
 Identities = 169/371 (45%), Positives = 242/371 (64%), Gaps = 9/371 (2%)

Query: 86 EYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWFAADF-SEKIGVPWIPVWTAASCS 144
 E F+ A P N+ A+ +A + G C LTD+FLWF D +E+ GVPWI WTA +CS

Sbjct: 12 EEFIMAMPNGNYQTAIAEAEAEAMGTFKGCFLTDSFLWFGGDLAAERGVPWISFWTAGACS 71

Query: 145 LCLHVTDEIRSRFAEFDIA--EKAETIDFIPGLSAISFSDDLPEELIMEDSQSIFALT 202
 + H+YTD +RS A A ++ + IPG+S +S ++P E++ +D Q+ F +

Sbjct: 72 ISAHLYTDFVRSIVAATPNANGNGLDQKLKVIPGMSEVSIGEMPGEILAKDLQAPFPGMI 131

Query: 203 HNMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILNIGPLQTLSSSIPP---EDNEC 259
 +NM LKL A A+ +NSF++++P +T+ LRS ++ + NIGP+ ++ P +D+ C
 Sbjct: 132 YNMALKLPGANALVLNSFQKLEPTVTDDLRS--KVQVFNIGPMILQPATPKPPISDDHNC 189

Query: 260 LKWLQT-QKESSVVYLSFGTVINPPPNEAALASTLESRKIPFLWSLRDEARKHLPENFI 318
 + WL + SS VYLSFG+ I PPP+E+ LA LE+++ PFLWSL+ KHLPE F+
 Sbjct: 190 IPWLDLPPASSAVYLSFGSGITPPPDEIVGLAKALEAKRAPFLWSLKPHGVKHLPEGFV 249

Query: 319 DRTSTFGKIVSWAPQLHVLNPAIGVFVTHCGWNSTLESIFCRVPVIGRPFFGDQKVNAR 378
 +RT FGKIV WAPQ+ VL +P +GVFVTHCGWNSTLE+I C V +I RPF+GDQK+N R
 Sbjct: 250 ERTKEFGKIVPWAPQVQLSHPGVGVFVTHCGWNSTLEAISCVCMICRPFYGDQKINTR 309

Query: 379 MVEDXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNVGRLKEKAKDAVKANGSST 438
 VE FT+D T + L +VL SD+GK +++NV +LK +A +AVK NGSST
 Sbjct: 310 FVESVWEIGVKIEGGIFTKDGTMKALNVVLDSRGLKLLKENVVKLKGEALEAVKPNGSST 369

Query: 439 RNFESLLAAFN 449
 ++F+ L+ N
 Sbjct: 370 KDFQELVHLLN 380

>gi|4588779|gb|AAD26203.1|AF117267.1 (AF117267) UDP glucose:flavonoid 3-O-glucosyl t
 domestica]
 Length = 483

Score = 338 bits (866), Expect = 7e-92

Identities = 189/450 (42%), Positives = 267/450 (59%), Gaps = 13/450 (2%)

Query: 6 HVAVLAFPFPGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIKP 65
 HVAV+AFPF +HA+ LL V RLA + P+ ++ ++ NI+ Y
 Sbjct: 27 HVAVVAFPFTHASALLETVRRLATALPNTLFSFFSTSKSNSSLFSNNSIDNMPNRIRVY 86

Query: 66 AVWDGSPEGVFVSGNPPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWF 125
 V DG PEG+VF G P+E IE F+NAAP+N +++ +V D G ISCL+TDAFLWF
 Sbjct: 87 DVADGVPEGYVFGKPKQEDIELFMNAAPENIRRSILDASVADIGKQISCLITDAFLWFGVH 146

Query: 126 FSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRAEFDAEK-----AEKTIDFIPGLSAI 180
 ++++GVPW+ W + SL +HV+TD IR I + +K ++ I GLS +
 Sbjct: 147 LADELGVPWVTFWISGLKSLSVHVTDLIRDITIGTQGITGRENDLIVDKNVN-IQGLSNV 205

Query: 181 SFSDLPEELIMEDSQSIFALTLHNMGLKLHKATAVAVNSFEEIDPIITNHLRS-TNQLNI 239
 DL E +I + S+ + L MG L +ATAV +N FEE++ I N L+S N+L
 Sbjct: 206 RIKDLAEGVIFGNLDSVISGMLLMGRLLPRATAVFMNGFEELELPIPNDLKSKVNKL-- 263

Query: 240 LNIGPLQ-TLSSSIPPEDNECKWLQTQKE-SSVVYLSFGTVINPPPNEAALASTLESR 297
 LN+GP P + CL WL Q+ SSVVY+SFGTV +P E A+A LE+
 Sbjct: 264 LNVGPSNVASPLPLPPSDACLSWLDKQAPSSVVYISFGTVASPAEKEQMAIAEALAT 323

Query: 298 KIPFLWSLRDEARKHLPENFIDRTST--FGKIVSWAPQLHVLNPAIGVFVTHCGWNSTL 355
 PFLWS++D + L F+ +T + G +V WAPQ HVL + ++G FV+HCGWNS +
 Sbjct: 324 GAPFLWSIKDSCKTPLLNEFLTTLKSLKNGMVVPWAPQPHVLAHDSVGAFVSHCGWNSIM 383

Query: 356 ESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKE 415
 E+I RVP+I RP+F DQ++NARMVE+ FT + + LE+VL + G++
 Sbjct: 384 ETIAGRVPMICRPYFADQRLNARMVEEVFEIGVTVEDGVFTREGLVKSLEVVLSPEGRK 443

Query: 416 MRQNVGRLKEKAKDAVKANGSSTRNFESLL 445
 R N+ R+K+ A +AV GSSTRNF+SLL
 Sbjct: 444 FRDNIKRVKQLAVEAVGPQGSSTRNFKSLL 473

>gi|2501498|sp|Q43641|UFOG SOLME FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVO
 3-O-GLUCOSYLTRANSFERASE)
 gi|1076656|pir||S51767 glycosyl transferase - eggplant
 gi|607192|emb|CAA54558.1| (X77369) glycosyl transferase [Solanum melongena]
 Length = 433

Score = 338 bits (866), Expect = 8e-92

Identities = 193/432 (44%), Positives = 257/432 (58%), Gaps = 24/432 (5%)

```

Query: 6  HVAVLAFPPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIPY 65
      H+A LAFPPFGTHA PLLTLV +++ P + NIK Y
Sbjct: 7  HIAFLAFPPFGTHATPLLTLLVQKISPFPLPSSTIFSFFNTSSSNSSIFSK--VPNQENIKIY 64

Query: 66 AVWDGSPEGFVFSGNP--REPIEYFLNAAPDNFDKAMKKAEDTGVNISCLLTDAFLW-F 122
      VWDG EG + P E I+ F+ + K ++A E+TGV SC+ +DAFLW F
Sbjct: 65 NVWDGVKEG---NDTPFGLEAIKLFIQSTL-LISKITEEAEETGVKFSCIFSDAFLWCF 120

Query: 123 AADFSEKIGVPWIPVWTAASCSLCLHVTYDEIRSRFAEFDIAEKAECTIDFIPGLSA-IS 181
      +K+ P + WT SCSL +H+YTD IRS ++T IPG S+ +S
Sbjct: 121 LVKLPKMKMNAPGVAYWTGGSCSLAVHLYTDLIRSN-----KETSLKIPGFSSTLS 170

Query: 182 FSDLPEELIMEDSQSIFALTTLHNMGLKLHKATAVAVNSFEEI--DPIITNHLRSTNQLNI 239
      +D+P E+ ED + + L+NM L LHKA AV +NSF+E+ DP+I L+ Q +
Sbjct: 171 INDIPPEVTAEDLEGPMSSMLYNMALNLHKADAVVLNSFQELDRDPLINKDLQKNLQ-KV 229

Query: 240 LNIGPLQTLSSSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKI 299
      NIGPL L SS +++ C++WL QKE SVVYLSFGTV PPNE+ ++A LE++K
Sbjct: 230 FNIGPL-VLQSSRKLDSESGCIQWLDKQKEKSVVYLSFGTVTTLPNEIGSIAEALETCKT 288

Query: 300 PFLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIF 359
      PF+WSLR+ K+LP+ F++RT FGKIVSWAPQL +L + ++GVFVTHCGWNS LE I
Sbjct: 289 PFIWSLRNNGVKNLPGKFLERTKEFGKIVSWAPQLEILAHKSVGVFVTHCGWNSILEGIS 348

Query: 360 CRVPVIGRPFPGDQKVNARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLFSDKKGKEMRQN 419
      VP+I RPFPGDQK+N+RMVE FT+ L+ +KGK +R+N
Sbjct: 349 FGVPMICRPFPGDQKLNRMVESVWEIGLQIEGGIFTKSGIISALDTFFNEEKGKILREN 408

Query: 420 VGRLEKEKAKDAV 431
      V LKEKA +AV
Sbjct: 409 VEGLKEKALEAV 420

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>gi|4140026|dbj|BAA36972.1| (AB009370) flavonoid 3-O-galactosyl transferase [Vigna m
Length = 455

Score = 312 bits (800), Expect = 4e-84

Identities = 176/450 (39%), Positives = 258/450 (57%), Gaps = 19/450 (4%)

```

Query: 6  HVAVLAFPPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLIS---IGSNI 62
      HVAV +FPFG+H PLL LV +L +AP+ LIS I I
Sbjct: 9  HVAVFSFPFGSHPTPLNLVLKLTNAAPNLQFSFIGTEHSNKSL-----LISKPHIPDTI 63

Query: 63 KPYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAEDTGVNISCLLTDAFLWF 122
      K Y++ DG PEG V G+P E + FL A+P N K + AV T ++C+++DAF+
Sbjct: 64 KFYSISDGVPEGHVPGGHPVERVNLFLQASPQNLQKGIDMAVAHTKERVTCVISDAFVAP 123

Query: 123 AADFSEKIGVPWIPVWTAASCSLCLHVTYDEIRSRFAEFDIAEKAECTIDFIPGLSAISF 182
      + ++++ VPW+PVW SCSL H YT+ IR + + +DF+PGLS +
Sbjct: 124 SLTVAQRLNVPWPVPVWPLSCSLSAHFYTELIRQTCN----SAAGDTPLDFVPGLSKMRV 179

Query: 183 SDLPEELIM--EDSQSIFALTTLHNMGLKLHKATAVAVNSFEEID-PIITNHLRSTNQ--- 236
      DLPE++I + +++F+ TL ++G L +A AV VN FEE+D P++ N ++S +
Sbjct: 180 EDLPEDVIQGAGEEETLFSKTLASLGSVLPQAEAVVNVFFEELDPPLLNDMKSFKFYLL 239

Query: 237 -LNILNIGPLQTLSSSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLE 295
      + L + ++ CL WL QK SVVY+SFGTV+ PPP+E+ A+A LE
Sbjct: 240 YVGFLTSLPLPLPPSDTDETGCLSWLDKQKGGSVVYVSFGTVVTPPPHEIVAVAEALE 299

Query: 296 SRKIPFLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTL 355
      + PFLWSL++ + LP F++RTS GK+V WAPQ VL + ++GVFVTHCG NS
Sbjct: 300 ASGFPPFLWSLKEHLKGVLPNGFLERTSERGKVVGWAPQTQVLGHGSVGVFVTHCGCNSVF 359

```


Query: 356 ESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKE 415
 ES+ VP+I RPFFGD + RMVED FT+D + L L+L ++G
 Sbjct: 360. ESMSGVPMICRPFFGDHGLTGMRVEDVWEIGVRVEGGVFTKDGLLKSRLRLILVEEEGNL 419

Query: 416 MRQNVGRLKEKAKDAVKANGSSSTRNFESLL 445
 M++N ++K+ DA A G + ++F +L+
 Sbjct: 420 MKKNVAVKVKKTVLDAAGAQAQKAAQDFNTLV 449

>gi|15237897|ref|NP_197206.1| UDP glucose:flavonoid 3-o-glucosyltransferase -like pr
 [Arabidopsis thaliana]
 gi|11358642|pir|T51559 probable flavonol 3-O-glucosyltransferase (EC 2.4.1.91) F2K
 [similarity] - Arabidopsis thaliana
 gi|9755705|emb|CAC01717.1| (AL391141) UDP glucose:flavonoid 3-o-glucosyltransferase
 protein [Arabidopsis thaliana]
 Length = 472

Score = 309 bits (791), Expect = 4e-83
 Identities = 170/430 (39%), Positives = 249/430 (57%), Gaps = 18/430 (4%)

Query: 21 LLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIKPYAVWDGSPGFFVFSGN 80
 +L + RLA +AP + NI+ + V DG PEG+V S N
 Sbjct: 50 ILAVTRRLATAAPSTVFSFLNTSQSNFSLSS----DLPPNIRVHDVSDGVPEGYVLSRN 105

Query: 81 PREPIEYFLNAAPDNFDKAMKKAEDTGVNISCLLTDAFLWFAADFSEKIGVPWIPVWTA 140
 P+E +E FL AAP+ F + + A + G ++C+LTDAF+WFA D + ++ V W+ WT+
 Sbjct: 106 PQEAVELFLEAAPEIFRRELAVAETEVRKVTCLMTDAFIWFAGDMAAEMKVSWSVAFWTS 165

Query: 141 ASCSLCLHVYTDEIRSRFAEFDIAEKAECTIDFIPGLSAISFSDLPEELIMEDSQSIFAL 200
 + SL + + +I S +++T+ I G+ I D PE ++ + S+F+
 Sbjct: 166 GTRSLLI---STQISSEKQSL-----SKETLGCISGMEKIRVKDTPEGVVFGNLDVSFVSK 217

Query: 201 TLHNMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILNIGPLQTLSSS----IPPED 256
 LH MGL L +AT V +NSFEE+DP +T++LR + L+IGPL L S+ P D
 Sbjct: 218 MLHQMGALPRATTVMNSFEELDPTLTDNRLRLKFK-RYLSIGPLALLFSTSQRETPLHD 276

Query: 257 -NECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWSLRDEARKHLPE 315
 + CL W++ + +SVVY++FG V+ PPP E+ +A LES K+PF+WSL+++ HLP+
 Sbjct: 277 PHGCLAWIKKRSTASVVYIAFGRVMTPPPGLVVAQGLESSKVPFVWSLQEKMMVHLPK 336

Query: 316 NFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRVPVIGRPFFGDQKV 375
 F+D T G +V WAPQ+ +L + A+GVFV+H GWNS LES+ VP+I RP FGD +
 Sbjct: 337 GFLDGTREQGMVVPWAPQVELLNHEAMGVFVSHGGWNSVLESVSAGVPMICRPFGDHAL 396

Query: 376 NARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNVGRLKEKAKDAVKANG 435
 NAR VE FT+D L+ VL D GK+M+ N +LKE A++AV G
 Sbjct: 397 NARSVEAVWEIGMTISSGVFTKDGFEESLDRVLVQDDGKKMKFNAKKLKELAQEAVSTEG 456

Query: 436 SSTRNFESLL 445
 SS NF+ LL
 Sbjct: 457 SSFENFKGLL 466

>gi|2501496|sp|Q40289|UFO7 MANES FLAVONOL 3-O-GLUCOSYLTRANSFERASE 7 (UDP-GLUCOSE FLA
 3-O-GLUCOSYLTRANSFERASE 7)
 gi|542017|pir|S41953 UTP-glucose glucosyltransferase - cassava
 gi|453253|emb|CAA54614.1| (X77464) UTP-glucose glucosyltransferase [Manihot esculen
 Length = 287

Score = 279 bits (713), Expect = 5e-74
 Identities = 137/276 (49%), Positives = 184/276 (66%), Gaps = 2/276 (0%)

Query: 170 TIDFIPGLSAISFSDLPEELIMEDSQSIFALTTLHNMGLKLHKATAVAVNSFEEIDPIITN 229
 T++ IPG+S I DLPE ++ + +S+F+ LHNMG L +A AV +NSFEE+DP I +
 Sbjct: 1 TLNLIPGMSKIQIRDLPEGVLFGNLESLSQMLHNMGRMLPRAAAVLMSFEELDPTIVS 60

Query: 230 HLRSTNQLNILNIGPLQTLSSSIP-PEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMA 288

L S NIL IGP +S P P+ C+ WL QK +SV Y+SFG+V PPP+E+
 Sbjct: 61 DLNSKFN-NILCIGPFNLVSPPPVPDITYGMAWLKQKQPASVAYISFGSVATPPPHLV 119
 Query: 289 ALASTLESRKIPFLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTH 348
 ALA LE+ K+PFLWSL+D ++ HLP F+DRT + G ++SWAPQ+ +LE+ A+GVFVTH
 Sbjct: 120 ALAAEALASKVPFLWSLKDHSKVHLPNGFLDRTKSHGIVLSWAPQVEILEHAALGVFVTH 179
 Query: 349 CGWNSTLESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXFTEDETTRVLELVL 408
 CGWNS LESI VP+I RPFFGDQ++N RMVED T++ L +L
 Sbjct: 180 CGWNSILESIVGGVPMICRPFFGDQRLNGRMVEDVWEIGLLMDGGVLTKNGAIDGLNQIL 239
 Query: 409 FSDKGKEMRQNVGRLKEKAKDAVKANGSSTRNFESL 444
 KGK+MR+N+ RLKE AK A + GSS+++F L
 Sbjct: 240 LQKGKMKMRENIKRLKELAKGATEPKGSSSKSFTEL 275

>gi|136743|sp|P16166|UFO1 MAIZE FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVON
 3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-MCC ALLELE)
 gi|82689|pir|S01052 flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (allele Bz-McC)
 maize
 gi|22205|emb|CAA30761.1| (X07940) UDPglucose flavonoid glycosyl-transferase [Zea ma
 gi|1030071|emb|CAA31855.1| (X13500) UDPglucose:flavonol 3-O-glucosyltransferase [Ze
 gi|14719287|gb|AAK73112.1|AF391808.2 (AF391808) UDPG-flavonoid 3-O-glucosyl transf
 Length = 471

Score = 226 bits (577), Expect = 3e-58

Identities = 163/461 (35%), Positives = 232/461 (49%), Gaps = 27/461 (5%)

Query: 2 SPVSHVAVLAFPPFGTHAAPLLTL-VNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIG- 59
 SP HVAV+AFPF +HAA LL++ AA+AP + S G
 Sbjct: 9 SPPPHVAVVAFPFSSHAALLSIALALAAAAPSGATLSFLSTASSLAQLRKASSASAGH 68
 Query: 60 ---SNIKPYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAM--KKAVEDTGVNISCL 114
 N++ V DG+P PR+ ++ F+ AA KA G ++C+
 Sbjct: 69 GLPGNLRFVEVPDGAPEETVPVPRQ-MQLFMEAAEAGGVKAWLEAARAAAGGARVTCV 127
 Query: 115 LTDAFLWFAADFSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEFDIAEKAECTIDFI 174
 + DAF+W AAD + G PW+PVWTAASC+L H+ TD +R D+ ++A +D +
 Sbjct: 128 VGDAFVWPAADAAASAGAPWVPVWTAASCALLAHIRTDALRE-----DVGDQAANRVDGL 182
 Query: 175 ----PGLSAISFSDLPEELIMEDSQSIFALT LHNMG LK LHK-ATAVAVNSFEEIDPIITN 229
 PGL++ DLP+ ++ D + L +H MG L + A AVA+N+F +DP
 Sbjct: 183 LISHPGLASYRVRDLDPDGVVSGDFNYVINLLVHRMGQCLPRSAVAALNTFPGLDPPDVT 242
 Query: 230 HLRSTNQLNINILNIGPLQTLSSS-----IPPEDNECLKWLQTQKESSVVYLSFGTVINPP 283
 + N + GP L + P + + CL WL Q V Y+SFGTV P
 Sbjct: 243 AALAEILPNCVPFPGPYHLLLAEDDADTAAPADPHGCLAWLGRQPARGVAYVSFGTVACPR 302
 Query: 284 PNEMAALASTLESRKIPFLWSLRDEARKHLPENFIDRTSTFGK--IVSWAPQLHVLENPA 341
 P+E+ LA+ LE PFLWSLR+++ HLP F+DR + G +V WAPQ+ VL +P+
 Sbjct: 303 PDELRELAAGLED SGAPFLWSLREDSWPHLPPGFLDRAAGTGSGLVVPWAPQVAVLRHPS 362
 Query: 342 IGVFVTHCGWNSTLESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXFTEDETT 401
 +G FVTH GW S LE + VP+ RPFFGDQ++NAR V + T
 Sbjct: 363 VGAFVTHAGWASVLEGLSSGVPMACRPFFGDQRMNARSVAHVWGFGAAGFEGAMTSAGVAT 422
 Query: 402 RVLELVLFSKDGKEMRQNVGRLKEKAKDAVKANGSSTRNFE 442
 V EL L ++G MR L+ +A G +NF+
 Sbjct: 423 AVEEL-LRGEEGARMRARAKELQALVAEAFGGGECRKNFD 462

>gi|13241668|gb|AAK16410.1|AF320086.2 (AF320086) UDPG-flavonoid 3-O-glucosyl transfe
 Length = 471

Score = 226 bits (577), Expect = 3e-58

Identities = 163/461 (35%), Positives = 232/461 (49%), Gaps = 27/461 (5%)

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Query: 2   SPVSHVAVLAFPPFGTHAAPLLTL-VNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIG- 59
          SP  HVAV+AFPF +HAA LL++      AA+AP                      + S G
Sbjct: 9   SPPPHVAVVAFPFSSHA AVL LSIARALAAAAAPSGATLSFLSTASSLAQLRKASSASAGH 68

Query: 60  ---SNIKPYAVWDGSPGEGFVFSGNPREPIEYFLNAAPDNFDKAM--KKAVEDTG VNI SCL 114
          N++   V DG+P          PR+ ++ F+ AA      KA          G ++C+
Sbjct: 69  GLPGNLRFVEVPDGAPAAEETVPVPRQ-MQLFMEAAEAGGVKAWLEAARAAAGGARVTCV 127

Query: 115  LTDAFLWFAADFSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEFDIAEKA EKTIDFI 174
          + DAF+W AAD +      G PW+PVWTAASC+L H+ TD +R          D+ ++A +D +
Sbjct: 128  VGDAFVWPAADAAASAGAPWVPVWTAASCALLAHIRTDALRE-----DVG DQAANRVDGL 182

Query: 175  ----PGLSAISFSDLPEELIMEDSQSIFALT LHN MGLKLHK-ATAVAVNSFEEIDPIITN 229
          PGL++   DLP+ ++ D   + L +H MG L + A AVA+N+F +DP
Sbjct: 183  LISHPGLASYRVRDLDPGVVSGDFNYVINLLVHRMGQCLPRSAAVALNTFPGLDPPDVT 242

Query: 230  HLRSTNQLNILNIGPLQTLSSS-----IPPEDNECLKWLQTQKESSVVYLSFGTVINPP 283
          +   N + GP L +          P + + CL WL Q   V Y+SFGTV P
Sbjct: 243  AALAEILPNCVPFGPYHLLLAEDDADTAAPADPHGCLAWLGRQPARGVAYVSFGTVACPR 302

Query: 284  PNEMAALASTLESRKIPFLWSLRDEARKHLPENFIDRTSTFGK--IVSWAPQLHVLENPA 341
          P+E+ LA+ LE      PFLWSLR+++ HLP F+DR + G   +V WAPQ+ VL +P+
Sbjct: 303  PDELRELAAGLED SGAPFLWSLRDSWPHLPPGF LDRAAGTGSGLVVPWAPQVAVLRHPS 362

Query: 342  IGVFVTHCGWNSTLESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETT 401
          +G FVTH GW S LE +   VP+ RPF FGDQ++NAR V          + T
Sbjct: 363  VGAFVTHAGWASVLEGLSSGVPMACRPFFGDQRMNARSVAHVWGFGAAFE GAMTSAGVAT 422

Query: 402  RVLELVLFSDKKGEMRQNVGRLKEKAKDAVKANGSSSTRNFE 442
          V EL L ++G MR      L+   +A   G   +NF+
Sbjct: 423  AVEEL-LRGEEGARMRARAKELQALVAEAFGPGGECRKNFD 462

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>gi|136744|sp|P16165|UFO2 MAIZE FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVON
3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-MC2 ALLELE)
gi|82692|pir|S08325 flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (allele BzMcc2)
maize
gi|295854|emb|CAA31856.1| (X13501) UFGT [Zea mays]
Length = 471

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Score = 220 bits (560), Expect = 2e-56

Identities = 160/461 (34%), Positives = 231/461 (49%), Gaps = 27/461 (5%)

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Query: 2   SPVSHVAVLAFPPFGTHAAPLLTL-VNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIG- 59
          SP  HVAV+AFPF +HAA LL++      AA+AP                      + S G
Sbjct: 9   SPPPHVAVVAFPFSSHA AVL LSIARALAAAAAPSGATLSFLSTASSLAQLRKASSASAGH 68

Query: 60  ---SNIKPYAVWDGSPGEGFVFSGNPREPIEYFLNAAPDNFDKAM--KKAVEDTG VNI SCL 114
          N++   V DG+P          PR+ ++ F+ AA      KA          G ++C+
Sbjct: 69  GLPGNLRFVEVPDGAPAAEETVPVPRQ-MQLFMEAAEAGGVKAWLEAARAAAGGARVTCV 127

Query: 115  LTDAFLWFAADFSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEFDIAEKA EKTID-- 172
          + DAF+W AAD +      G PW+PVWTAASC+L H+ TD +R          D+ ++A +D
Sbjct: 128  VGDAFVWPAADAAASAGAPWVPVWTAASCALLAHIRTD SLRE-----DVG DQAANRVD EP 182

Query: 173  --FIPGLSAISFSDLPEELIMEDSQSIFALT LHN MGLKLHK-ATAVAVNSFEEIDPIITN 229
          PGL++   DLP+ ++ D   +L +H MG L + A AVA+N+F +DP
Sbjct: 183  LISHPGLASYRVRDLDPGVVSGDFNYVISLLVHRMGQCLPRSAAVALNTFPGLDPPDVT 242

Query: 230  HLRSTNQLNILNIGPLQTLSSS-----IPPEDNECLKWLQTQKESSVVYLSFGTVINPP 283
          +   N + GP L +          P + + CL WL Q   V Y+SFGTV P
Sbjct: 243  AALAEILPNCVPFGPYHLLLAEDDADTAAPADPHGCLAWLGRQPARGVAYVSFGTVACPR 302

Query: 284  PNEMAALASTLESRKIPFLWSLRDEARKHLPENFIDRTSTFGK--IVSWAPQLHVLENPA 341
          P+E+ LA+ LE+      PFLWSLR+++ LP F+DR + G   +V WAPQ+ VL +P+
Sbjct: 303  PDELRELAAGLEASAAPFLWSLRDSWTLPPGF LDRAAGTGSGLVVPWAPQVAVLRHPS 362

```

Query: 342 IGVFVTHCGWNSTLESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETT 401
 +G FVTH GW S LE + VP+ RPFFGDQ++NAR V T
 Sbjct: 363 VGAFVTHAGWASVLEGVSSGVPMACRPFFGDQRMNARSVA-HVWGFGAAFEGAMTSAGVA 421

Query: 402 RVLELVLFSDKGKEMRQNVGRLKEKAKDAVKANGSSTRNFE 442
 +E +L ++G MR L+ +A G +NF+
 Sbjct: 422 AAVEELLRGEAGMRARAKELQALVAEAFGPGGECRKNFD 462

>gi|136745|sp|P16167|UFO3 MAIZE FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVON
 3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-W22 ALLELE)
 gi|82690|pir|S01037 flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (allele Bz-W22)
 maize
 gi|22210|emb|CAA30760.1| (X07937) UDPglucose flavonoid glycosyl transferase [Zea ma
 gi|22506|emb|CAA31857.1| (X13502) UFGT (AA 1 - 471) [Zea mays]
 Length = 471

Score = 219 bits (557), Expect = 6e-56
 Identities = 160/461 (34%), Positives = 230/461 (49%), Gaps = 27/461 (5%)

Query: 2 SPVSHVAVLAFPPFGTHAAPLLTL-VNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIG- 59
 SP HVAV+AFPF +HAA LL++ AA+AP + S G
 Sbjct: 9 SPPPHVAVVAFPFSSHAALLSIARALAAAAPSGATLSFLSTASSLAQLRKASSASAGH 68

Query: 60 ---SNIKPYAVWDGSPGFFVFSGNPREPIEYFLNAPDNFDKAM--KKAVEDTGVNISCL 114
 N++ V DG+P PR+ ++ F+ AA KA G ++C+
 Sbjct: 69 GLPGNLRFEVVPDGPAAEESVPVPRQ-MQLFMEAAEAGGVKAWLEAARAAAGGARVTCV 127

Query: 115 LTDAFLWFAADFSEKIGVPWIPVWTAASCSLCLHVYTDEIRSFAEFDIAEKAECTID-- 172
 + DAF+W AAD + G PW+PVWTAASC+L H+ TD +R D+ ++A +D
 Sbjct: 128 VGDAFVWPAADAAASAGAPWVPVWTAASCALLAHIRTDALRE-----DVGDQAANRVDEP 182

Query: 173 --FIPGLSAISFSDLPEELIMEDSQSIFALTLHNMGLKLHK-ATAVAVNSFEEIDPIITN 229
 PGL++ DLP+ ++ D + L +H MG L + A AVA+N+F +DP
 Sbjct: 183 LISHPGLASYRVRDLDPGVVSGDFNYVINLLVHRMGQCLPRSAVALNTFPGLDPPDVT 242

Query: 230 HLRSTNQLNILNIGPLQTLSSS-----IPPEDNECLKWLQTQKESSVVYLSFGTVINPP 283
 + N + GP L + P + + CL WL Q V Y+SFGTV P
 Sbjct: 243 AALAEILPNCVPFGPYHLLLAEDDADTAAPADPHGCLAWLGRQPARGVAVVSFGTVACPR 302

Query: 284 PNEMAALASTLESRKIPFLWSLRDEARKHLPENFIDRTSTFGK--IVSWAPQLHVLENPA 341
 P+E+ LA+ LE+ PFLWSLR+++ LP F+DR + G +V WAPQ+ VL +P+
 Sbjct: 303 PDELRELAAGLEASGAPFLWSLRSDSWTLLPPGFLDRAAGTGSGLVVPWAPQVAVLRHPS 362

Query: 342 IGVFVTHCGWNSTLESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETT 401
 +G FVTH GW S LE + VP+ RPFFGDQ++NAR V T
 Sbjct: 363 VGAFVTHAGWASVLEGVSSGVPMACRPFFGDQRMNARSVA-HVWGFGAAFEGAMTSAGVA 421

Query: 402 RVLELVLFSDKGKEMRQNVGRLKEKAKDAVKANGSSTRNFE 442
 +E +L ++G MR L+ +A G +NF+
 Sbjct: 422 AAVEELLRGEAGMRARAKVLQALVAEAFGPGGECRKNFD 462

>gi|136746|sp|P14726|UFOG HORVU FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVON
 3-O-GLUCOSYLTRANSFERASE) (BRONZE-1)
 gi|66580|pir|XUBHFG flavonol 3-O-glucosyltransferase (EC 2.4.1.91) - barley
 gi|295807|emb|CAA33729.1| (X15694) UDPglucose flavonol 3,0 glucosyl transferase [Ho
 vulgare]
 Length = 455

Score = 207 bits (526), Expect = 2e-52
 Identities = 150/454 (33%), Positives = 218/454 (47%), Gaps = 19/454 (4%)

Query: 3 PVSHVAVLAFPPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNI 62
 P H+AV+AFPF +HAA L + LAA+AP ++ N+
 Sbjct: 4 PPPHIAVAVFPFSSHAALLSFARALAAAAPAGTSLSFLTTADNAAQLRKAG--ALPGNL 61